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#2   OIPE

RAW SEQUENCE LISTING   DATE: 01/16/2002
PATENT APPLICATION: US/09/993,234   TIME: 18:33:08

Input Set : N:\Crf3\RULE60\09993234.raw
Output Set: N:\CRF3\01162002\I993234.raw

SEQUENCE LISTING

```
 3 (1) GENERAL INFORMATION:
 5      (i) APPLICANT: Ashkenazi, Avi J.
 7     (ii) TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
 9    (iii) NUMBER OF SEQUENCES: 11
11     (iv) CORRESPONDENCE ADDRESS:
12          (A) ADDRESSEE: Genentech, Inc.
13          (B) STREET: 460 Point San Bruno Blvd
14          (C) CITY: South San Francisco
15          (D) STATE: California
16          (E) COUNTRY: USA
17          (F) ZIP: 94080
19      (v) COMPUTER READABLE FORM:
20          (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
21          (B) COMPUTER: IBM PC compatible
22          (C) OPERATING SYSTEM: PC-DOS/MS-DOS
23          (D) SOFTWARE: WinPatin (Genentech)
25     (vi) CURRENT APPLICATION DATA:
26          (A) APPLICATION NUMBER: US/09/993,234      C-->
27          (B) FILING DATE: 19-Nov-2001              C-->
28          (C) CLASSIFICATION:
30    (vii) PRIOR APPLICATION DATA:
31          (A) APPLICATION NUMBER: 08/828,683
32          (B) FILING DATE:
36   (viii) ATTORNEY/AGENT INFORMATION:
37          (A) NAME: Marschang, Diane L.
38          (B) REGISTRATION NUMBER: 35,600
39          (C) REFERENCE/DOCKET NUMBER: P1007P1
41     (ix) TELECOMMUNICATION INFORMATION:
42          (A) TELEPHONE: 415/225-5416
43          (B) TELEFAX: 415/952-9881
44          (C) TELEX: 910/371-7168
46 (2) INFORMATION FOR SEQ ID NO: 1:
48      (i) SEQUENCE CHARACTERISTICS:
49          (A) LENGTH: 181 amino acids
50          (B) TYPE: Amino Acid
51          (D) TOPOLOGY: Linear
53     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
55 Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu
56   1               5                  10                  15
58 Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser
59                  20                  25                  30
61 Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu
62                  35                  40                  45
64 Phe Cys Cys Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro
65                  50                  55                  60
67 Cys Thr Glu Pro Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln
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```
68                  65              70              75
70  Asp Thr Phe Leu Ala Trp Glu Asn His His Asn Ser Glu Cys Ala
71                  80              85              90
73  Arg Cys Gln Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu
74                  95              100             105
76  Asn Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro Gly
77                  110             115             120
79  Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser Ser Ser Pro
80                  125             130             135
82  Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly Ala Leu His Arg His
83                  140             145             150
85  Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr Asp Cys Gly Thr Cys
86                  155             160             165
88  Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys Val Ser Cys Pro
89                  170             175             180
91  Thr
92  181
94  (2) INFORMATION FOR SEQ ID NO: 2:
96      (i) SEQUENCE CHARACTERISTICS:
97          (A) LENGTH: 433 base pairs
98          (B) TYPE: Nucleic Acid
99          (C) STRANDEDNESS: Single
100          (D) TOPOLOGY: Linear
102     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
105  CTGCTGGGGG CCCGGGCCAG NGGCGGCACT CGTAGCCCCA GGTGTGACTG 50
107  TGCCGGTGAC TTCCACAAGA AGATTGGTCT GTTTTGTTGC AGAGGCTGCC 100
109  CAGCGGGGCA ACTACCTGAA GGCCCCTTGC ACGGAGCCCT GCGCAACTCC 150
111  ACCTGCCTTG TGTGTCCCCA AGACACCTTC TTGGCCTGGG AGAACCACCA 200
113  TAATTCTGAA TGTGCCCGCT GCCAGGCCTG TGATGAGCAG GCCTCCCAGG 250
115  TGGCGCTGGA GAACTGTTCA GCAGTGGCCG ACACCCGCTG TGGCTGTAAG 300
117  CAGGGCTGGT TTGTGGAGTG CCAGGGTCAG CCAATGTGTC AGCAGTTTCA 350
119  CCCTTCTAAT GCCAACCATG CCTAGACTGC GGGGCCCTGC AACGCAACAC 400
121  ACGGCTAATN TGTTTCCCGC AGAGATNATT GTT 433
123  (2) INFORMATION FOR SEQ ID NO: 3:
125      (i) SEQUENCE CHARACTERISTICS:
126          (A) LENGTH: 28 base pairs
127          (B) TYPE: Nucleic Acid
128          (C) STRANDEDNESS: Single
129          (D) TOPOLOGY: Linear
131     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
134  CCCGCTGCCA GGCCTGTGAT GAGCAGGC 28
136  (2) INFORMATION FOR SEQ ID NO: 4:
138      (i) SEQUENCE CHARACTERISTICS:
139          (A) LENGTH: 28 base pairs
140          (B) TYPE: Nucleic Acid
141          (C) STRANDEDNESS: Single
142          (D) TOPOLOGY: Linear
144     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
147  CAGGGCCCCG CAGTCTAGGC ATGGTTGG 28
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```
149 (2) INFORMATION FOR SEQ ID NO: 5:
151      (i) SEQUENCE CHARACTERISTICS:
152           (A) LENGTH: 1438 base pairs
153           (B) TYPE: Nucleic Acid
154           (C) STRANDEDNESS: Single
155           (D) TOPOLOGY: Linear
157      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
160  GAATTCCGGC GCGGAGGCCG AGAGAGAAGT CACTTGCCCT GGCTCTACCT 50
162  TGAAGTGGTT CTCAGGGTTG GGGCGAGAGT CGGGGTGGGG ACCGAGATGC 100
164  AGCTCTATCC TGTGCCCCTG GTCGCAGCAG GCAGCCCAGC GCTTCGCGTG 150
166  TTCTACTTGG CCTGTCCGCT GCCGCCTAAT GAGCTCAGGT CTAGGCCGAG 200
168  CAGAGGGGGC ACCTGGTCGG ACTCGGTTGG GCTCGGGCGG CCCCGCCTCC 250
170  CCCCGCCCGC CAGGCGGGCC CTTCTCGACG GCGCGGGGCG GGCCCTGCGG 300
172  GCGCGGGGCT GAAGGCGGAA CCACGACGGG CAGAGAGCAC GGAGCCGGGA 350
174  AGCCCCTGGG CGCCCGTCGG AGGGCTATGG AGCAGCGGCC GCGGGGCTGC 400
176  GCGGCGGTGG CGGCGGCGCT CCTCCTGGTG CTGCTGGGGG CCCGGGCCCA 450
178  GGGCGGCACT CGTAGCCCCA GGTGTGACTG TGCCGGTGAC TTCCACAAGA 500
180  AGATTGGTCT GTTTTGTTGC AGAGGCTGCC CAGCGGGGCA CTACCTGAAG 550
182  GCCCCTTGCA CGGAGCCCTG CGGCAACTCC ACCTGCCTTG TGTGTCCCCA 600
184  AGACACCTTC TTGGCCTGGG AGAACCACCA TAATTCTGAA TGTGCCCGCT 650
186  GCCAGGCCTG TGATGAGCAG GCCTCCCAGG TGGCGCTGGA GAACTGTTCA 700
188  GCAGTGGCCG ACACCCGCTG TGGCTGTAAG CCAGGCTGGT TTGTGGAGTG 750
190  CCAGGTCAGC CAATGTGTCA GCAGTTCACC CTTCTACTGC CAACCATGCC 800
192  TAGACTGCGG GGCCCTGCAC CGCCACACAC GGCTACTCTG TTCCCGCAGA 850
194  GATACTGACT GTGGGACCTG CCTGCCTGGC TTCTATGAAC ATGGCGATGG 900
196  CTGCGTGTCC TGCCCCACGT AATTCCTAGC TGTCGTGGGA TGGAGGGAAG 950
198  GGCGGCTGGG AGCAGAGCAG GGGCCTGGGG TGGGGCAGGT GCTGCTGGTT 1000
200  CAGGAATAGG AAGAGGGGAT AGGGAGGAGG GAGCCTTGGC CCTGTGATGG 1050
202  GTGGGCCCCA CTTCAGGCAA ACTTAGATGG CAAAAGAGCA ATCTGGATCC 1100
204  GCCTTAGCCA GATACATAAG GGTATTTGCC TTCACTTTCA GCCAGCATTC 1150
206  CCCCCAGCGA TCCTAGCCAG ATATTACAGA TGATTTGTCA CTTACACAGA 1200
208  GAGTCACATT GATATAGCTT TAAAACTTGG GCTGAAGGAG GTTGAGGCTG 1250
210  CAGTGAGCTA TGATCGTGCC ACTGCACTTC AGCCTGGGCA ACAGAGCGAG 1300
212  ACCTATTAAA TAAATAAATA AATATTAAAT CTATTAAATA TTAAATATTA 1350
214  AATCTATTAA ATAAATAAAT ACAAAGGGCT GAGAGTCAGG ACTGTGCTGC 1400
216  TAGTTCTCTA GGGGATCTTG GGCAAGTGCA GAGAATTC 1438
218 (2) INFORMATION FOR SEQ ID NO: 6:
220      (i) SEQUENCE CHARACTERISTICS:
221           (A) LENGTH: 417 amino acids
222           (B) TYPE: Amino Acid
223           (D) TOPOLOGY: Linear
225      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
227  Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu
228  1            5                10                15
230  Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser
231              20                25                30
233  Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu
234              35                40                45
236  Phe Cys Cys Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro
```

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237                     50              55                  60
239   Cys Thr Glu Pro Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln
240                     65              70                  75
242   Asp Thr Phe Leu Ala Trp Glu Asn His His Asn Ser Glu Cys Ala
243                     80              85                  90
245   Arg Cys Gln Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu
246                     95              100                 105
248   Asn Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro Gly
249     .                110              115                 120
251   Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser Ser Ser Pro
252                     125              130                 135
254   Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly Ala Leu His Arg His
255                     140              145                 150
257   Thr Arg Leu Leu Cys Ser Arg Arg Asp Thr Asp Cys Gly Thr Cys
258                     155              160                 165
260   Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys Val Ser Cys Pro
261                     170              175                 180
263   Thr Ser Thr Leu Gly Ser Cys Pro Glu Arg Cys Ala Ala Val Cys
264                     185              190                 195
266   Gly Trp Arg Gln Met Phe Trp Val Gln Val Leu Leu Ala Gly Leu
267                     200              205                 210
269   Val Val Pro Leu Leu Leu Gly Ala Thr Leu Thr Tyr Thr Tyr Arg
270                     215              220                 225
272   His Cys Trp Pro His Lys Pro Leu Val Thr Ala Asp Glu Ala Gly
273                     230              235                 240
275   Met Glu Ala Leu Thr Pro Pro Pro Ala Thr His Leu Ser Pro Leu
276                     245              250                 255
278   Asp Ser Ala His Thr Leu Leu Ala Pro Pro Asp Ser Ser Glu Lys
279                     260              265                 270
281   Ile Cys Thr Val Gln Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr
282                     275              280                 285
284   Pro Glu Thr Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp
285                     290              295                 300
287   Asp Gln Leu Pro Ser Arg Ala Leu Gly Pro Ala Ala Ala Pro Thr
288                     305              310                 315
290   Leu Ser Pro Glu Ser Pro Ala Gly Ser Pro Ala Met Met Leu Gln
291                     320              325                 330
293   Pro Gly Pro Gln Leu Tyr Asp Val Met Asp Ala Val Pro Ala Arg
294                     335              340                 345
296   Arg Trp Lys Glu Phe Val Arg Thr Leu Gly Leu Arg Glu Ala Glu
297                     350              355                 360
299   Ile Glu Ala Val Glu Val Glu Ile Gly Arg Phe Arg Asp Gln Gln
300                     365              370                 375
302   Tyr Glu Met Leu Lys Arg Trp Arg Gln Gln Pro Ala Gly Leu
303                     380              385                 390
305   Gly Ala Val Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys
306                     395              400                 405
308   Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro
309                     410              415      417
```

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```
311 (2) INFORMATION FOR SEQ ID NO: 7:
313       (i) SEQUENCE CHARACTERISTICS:
314           (A) LENGTH: 27 base pairs
315           (B) TYPE: Nucleic Acid
316           (C) STRANDEDNESS: Single
317           (D) TOPOLOGY: Linear
319      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
322  GGCGCTCTGG TGGCCCTTGC AGAAGCC 27
324 (2) INFORMATION FOR SEQ ID NO: 8:
326       (i) SEQUENCE CHARACTERISTICS:
327           (A) LENGTH: 25 base pairs
328           (B) TYPE: Nucleic Acid
329           (C) STRANDEDNESS: Single
330           (D) TOPOLOGY: Linear
332      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
335  TTCGGCCGAG AAGTTGAGAA ATGTC 25
337 (2) INFORMATION FOR SEQ ID NO: 9:
339       (i) SEQUENCE CHARACTERISTICS:
340           (A) LENGTH: 1634 base pairs
341           (B) TYPE: Nucleic Acid
342           (C) STRANDEDNESS: Single
343           (D) TOPOLOGY: Linear
345      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
348  CGGGCCCTGC GGGCGCGGGG CTGAAGGCGG AACCACGACG GGCAGAGAGC 50
350  ACGGAGCCGG GAAGCCCCTG GGCGCCCGTC GGAGGGCT    ATG GAG 94
351                                              Met Glu
352                                               1
354  CAG CGG CCG CGG GGC TGC GCG GCG GTG GCG GCG GCG CTC 133
355  Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu
356          5                  10                  15
358  CTC CTG GTG CTG CTG GGG GCC CGG GCC CAG GGC GGC ACT 172
359  Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr
360                  20                  25
362  CGT AGC CCC AGG TGT GAC TGT GCC GGT GAC TTC CAC AAG 211
363  Arg Ser Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys
364          30                  35                  40
366  AAG ATT GGT CTG TTT TGT TGC AGA GGC TGC CCA GCG GGG 250
367  Lys Ile Gly Leu Phe Cys Cys Arg Gly Cys Pro Ala Gly
368                  45                  50
370  CAC TAC CTG AAG GCC CCT TGC ACG GAG CCC TGC GGC AAC 289
371  His Tyr Leu Lys Ala Pro Cys Thr Glu Pro Cys Gly Asn
372  55                  60                  65
374  TCC ACC TGC CTT GTG TGT CCC CAA GAC ACC TTC TTG GCC 328
375  Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala
376          70                  75                  80
378  TGG GAG AAC CAC CAT AAT TCT GAA TGT GCC CGC TGC CAG 367
379  Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln
380                  85                  90
382  GCC TGT GAT GAG CAG GCC TCC CAG GTG GCG CTG GAG AAC 406
```

VERIFICATION SUMMARY   DATE: 01/16/2002
PATENT APPLICATION: **US/09/993,234**   TIME: 18:33:09

Input Set : **N:\Crf3\RULE60\09993234.raw**
Output Set: **N:\CRF3\01162002\I993234.raw**

L:26 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:27 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:480 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:9